CLAIMS

What is claimed is:

1.   A method for identifying bi-nuclear cells, comprising:

capturing at least a first image of a plurality of marked cells;

processing the first image to obtain at least a first feature for each of the plurality of cells;

analyzing the first features for the plurality of cells to determine whether the first feature is indicative of a bi-nuclear cell; and

identifying those cells for which the first feature is indicative of a bi-nuclear cell as being a bi-nuclear cell.

2.   The method as claimed in claim 1, in which the first feature is a nuclear feature.

3.   The method as claimed in claim 2, in which the first feature is a nuclear morphology.

4.   The method as claimed in claim 3, in which analyzing the nuclear morphology further includes determining the number of nuclei present in the first feature.

5.   The method as claimed in claim 4, in which analyzing the nuclear morphology includes identifying concave regions in the periphery of the shape of the nuclear feature.

6.   The method as claimed in claim 5, in which cells are identified as being bi-nuclear if more than one concave region is identified.

7.   The method as claimed in claim 2, in which analysing the first feature further includes analysing the spatial distribution of the first feature.

8.   The method as claimed in claim 7, in which analysing the first feature further includes identifying at least one pair of first features.

9.   The method as claimed in claim 8, further including:

processing the first image to obtain a second feature indicative of a cytoplasmic component; and

wherein analyzing further comprises assessing the cytoplasmic component between the pair of first features.

10. The method as claimed in claim 9, in which identifying further comprises determining whether the amount of the cytoplasmic component exceeds a threshold value.

11. The method as claimed in claim 10, in which the threshold value relates to a control group of cells.

12. The method as claimed in claim 7, and further comprising identifying pairs of nearest neighbour first features.

13. The method as claimed in claim 12, and further comprising identifying the next nearest neighbour first features to a pair of nearest neighbour first features.

14. The method as claimed in claim 13, and further comprising identifying cells as being bi-nuclear when the pair of nearest neighbours are separated by less than a first threshold and the pair of nearest neighbours are separated from the next nearest neighbours by more than a second threshold.

15. A computer program product comprising a machine readable medium on which is provided program instructions for identifying bi-nuclear cells from a captured image of a plurality of marked cells, the instructions comprising:

code for processing the first image to obtain at least a first feature for each of the plurality of cells;

code for analyzing the first features for the plurality of cells to determine whether the first feature is indicative of a bi-nuclear cell; and

code for identifying those cells for which the first feature is indicative of bi-nuclear cells as being bi-nuclear cells.

16.   A computing device comprising a memory device configured to store at least temporarily program instructions for identifying bi-nuclear cells from a captured image of a plurality of marked cells, the instructions comprising:

    code for processing the first image to obtain at least a first feature for each of the plurality of cells;

    code for analyzing the first features for the plurality of cells to determine whether the first feature is indicative of a bi-nuclear cell; and

    code for identifying those cells for which the first feature is indicative of a bi-nuclear cell as being bi-nuclear cells.

17.   A method for assessing the affect of a treatment on a cell, comprising:

    exposing a population of cells to the treatment;

    capturing an image of a plurality of cells from the population;

    obtaining a plurality of cellular features from the image;

    analyzing the plurality of cellular features to assess a property of the cellular feature characteristic of bi-nuclear cells; and

    determining the abundance of bi-nuclear cells.

18.   A method as claimed in claim 17, and further comprising classifying the treatment based on the abundance of bi-nuclear cells.

19.   A method as claimed in claim 17, in which the plurality of cellular features includes nuclear features.

20.   A method as claimed in claim 19, in which the plurality of cellular features further includes cytoplasmic features.

21.   A method as claimed in claim 18, wherein the treatment is classified in terms of its affect on cytokinesis.

22.   A method as claimed in claim 18, further comprising applying a statistical test to the abundance of bi-nuclear cells in the treated cell population and the abundance of bi-nuclear cells in a control population in order to determine the significance of the affect of the treatment on the treated cell population.

23. A method for characterising cells, comprising:

determining, from a captured image of a nuclear component of a plurality of cells, the number of concave portions in the outline of the image of the nuclear component; and characterising the cell based on the number of concave portions.

24. The method as claimed in claim 23, further comprising smoothing the outline of the image of the nuclear component.

25. The method as claimed in claim 23, further comprising identifying a concave portion in the outline of the image of the nuclear component by determining the angle subtended by adjacent portions of the outline.

26. The method as claimed in claim 25, wherein identifying a concave portion further includes determining whether the angle is less than a threshold angle.

27. The method as claimed in claim 24, wherein smoothing the outline of the image of the nuclear component includes converting the outline into a polygon.

28. The method as claimed in claim 23, wherein the cell is characterised based on the number of concave portions identified and a secondary criterion

29. The method as claimed in claim 28, wherein the secondary criterion is indicative of the amount of nuclear material.

30. The method as claimed in claim 23, wherein the cell is characterised as multi-nuclear if more than two concave portions are identified.

31. The method as claimed in claim 23, wherein characterising the cell further includes assessing a further feature of a nuclear image of the nuclear component

32. The method as claimed in claim 31, wherein the further feature of the image of the nuclear component is the total intensity of the image of the nuclear component.

33. The method as claimed in claim 32, wherein the cell is characterised as multinucleate if there are two or more concave portions and the total intensity exceeds a first threshold.

34. The method as claimed in claim 33, wherein the cell is characterized as bi-nuclear if the cell is not characterised as multi-nuclear and has more than one concave portion and the total intensity exceeds a second threshold which is less than the first threshold.

35. A computer program product comprising a machine readable medium on which is provided program instructions for characterising cells, the instructions comprising:

code for determining, from a captured image of a nuclear component of a plurality of cells, the number of concave portions in the outline of the image of the nuclear component; and

code for characterising the cell based on the number of concave portions.

36. A computing device comprising a memory device configured to store at least temporarily program instructions for characterising cells, the instructions comprising:

code for determining, from a captured image of a nuclear component of a plurality of cells, the number of concave portions in the outline of the image of the nuclear component; and

code for characterising the cell based on the number of concave portions.

37. A method of identifying bi-nuclear cells, comprising:

identifying, from a captured image of a nuclear component of a plurality of cells, at least one pair of nuclear components;

determining, from a captured image of a cytoplasmic component of the plurality of cells, a measure of the amount of the cytoplasmic component interposed between the pair of nuclear components; and

characterising the cells based on the measure of the amount of the cytoplasmic component.

38. The method as claimed in claim 37, wherein the measure is the detected intensity of the image of the cytoplasmic component.

39.   The method as claimed in claim 38, further including:

identifying a straight path between the pair of nuclear components; and

determining the amount of the cytoplasmic component that falls under the path.

40.   The method as claimed in claim 39, wherein the path extends between the centroids of the pair of nuclear components.

41.   The method as claimed in claim 40, wherein the amount of cytoplasmic component is determined by summing over the path extending between the peripheries of the nuclear components.

42.   The method as claimed in claim 37, wherein a pair of nuclear components is identified as a pair, if the nuclear components are mutual nearest neighbours.

43.   The method as claimed in claim 37, further including removing particular nuclear components from the image prior to identifying pairs.

44.   The method as claimed in claim 43, wherein the particular nuclear components are selected from the group comprising: nuclear components of mitotic cells; nuclear components it the edge of the image; multinucleate nuclear components; nuclear components having an image intensity exceeding a threshold; and nuclear components having an image intensity below a threshold.

45.   The method as claimed in claim 37, wherein characterising the cells further includes comparing the measure of the amount of the cytoplasmic component with a measure of the amount of the same cytoplasmic component for a control group of cells.

46.   The method as claimed in claim 45, wherein the measure of the amount for the control group corresponds to the proportion of bi-nuclear cells expected in the control group.

47.   The method as claimed in claim 46, wherein the proportion of bi-nuclear cells expected in the control group is not more than 4%.

48.   A computer program product comprising a machine readable medium on which is provided program instructions for identifying bi-nuclear cells, the instructions comprising:

code for identifying, from a captured image of a nuclear component of a plurality of cells, at least one pair of nuclear components;

code for determining, from a captured image of a cytoplasmic component of the plurality of cells, a measure of the amount of the cytoplasmic component interposed between the pair of nuclear components; and

code for characterising the cells based on the measure of the amount of the cytoplasmic component.

49.   A computing device comprising a memory device configured to store at least temporarily program instructions for identifying bi-nuclear cells, the instructions comprising:

code for identifying, from a captured image of a nuclear component of a plurality of cells, at least one pair of nuclear components;

code for determining, from a captured image of a cytoplasmic component of the plurality of cells, a measure of the amount of the cytoplasmic component interposed between the pair of nuclear components; and

code for characterising the cells based on the measure of the amount of the cytoplasmic component.

50.   A method for identifying biologically relevant pairs of nuclei, comprising:

identifying, from a captured image of a nuclear component of a plurality of cells, at least one pair of nuclear components;

identifying, from the captured image, a nearest neighbour nuclear component to the pair of nuclear components; and

characterising the cells associated with the pair of nuclear components based on the separation of the pair of nuclear components and the separation of the next nearest neighbour nuclear component from the pair of nuclear components.

51.   The method as claimed in claim 50, wherein characterising the cell includes determining if the separation of the pair of nuclear components is less than a first threshold and the separation of the next nearest neighbour nuclear component and pair of nuclear components is greater than a second threshold.

52.   The method as claimed in claim 51, wherein the second threshold is at least twice the first threshold.

53.   The method as claimed in claim 51, wherein the separation between the pair of nuclear components is the shortest distance between the outlines of the nuclear components.

54.   The method as claimed in claim 50, further comprising identifying a set of candidate pairs of nuclear components.

55.   The method as claimed in claim 54, wherein identifying the set of candidate nuclear components includes determining the separation between the centroids of the nuclear components for each of the candidate pairs.

56.   The method as claimed in claim 51 wherein the first and second thresholds are computed based on the density of nuclear components in the captured image.

57.   The method as claimed in claim 51, wherein the cell associated with the pair of nuclear components is characterised as bi-nuclear if the separation of the pair of nuclear components is determined to be less than the first threshold and the separation of the next nearest neighbour nuclear component and pair of nuclear components is determined to be greater than the second threshold.

58.   The method as claimed in claim 57, further comprising determining the proportion of bi-nuclear cells in the captured image.

59.   A computer program product comprising a machine readable medium on which is provided program instructions for identifying biologically relevant pairs of nuclei, the instructions comprising:
        (a) code for identifying, from a captured image of a nuclear component of a plurality of cells, at least one pair of nuclear components;
        (b) code for identifying, from the captured image, a nearest neighbour nuclear component to the pair of nuclear components; and

(c) code for characterising the cell associated with the pair of nuclear components based on the separation of the pair of nuclear components and the separation of the next nearest neighbour nuclear component from the pair of nuclear components.

60.   A computing device comprising a memory device configured to store at least temporarily program instructions for identifying biologically relevant pairs of nuclei , the instructions comprising:

code for identifying, from a captured image of a nuclear component of a plurality of cells, at least one pair of nuclear components;

code for identifying, from the captured image, a nearest neighbour nuclear component to the pair of nuclear components; and

code for characterising the cell associated with the pair of nuclear components based on the separation of the pair of nuclear components and the separation of the next nearest neighbour nuclear component from the pair of nuclear components.